A case study on *Aspergillus* section *Nigri*: Identification and Characterisation of Fungal Strains from Nature

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Species of *Aspergillus* section *Nigri* have been extensively used for various biotechnological purposes and are among the fungi best studied which cause biodeterioration of commodities and food. Recently, *Aspergillus ibericus* (Serra *et al.*, 2006) and *Aspergillus uvarum* (Perrone *et al.*, 2008) were described as new species within the section and which were isolated from grapes. These new species were not only separated from others in the section by morphology, but were also with molecular characters. Additionally, some strains of black aspergilli can be mycotoxigenic (*e.g.* ochratoxin A) which can contaminate food and industrial commodities such as wine and citric acid. The identification of species is a fundamental goal in taxonomic microbiology. Information about each microorganism (*e.g.* morphological description, physiological and biochemical properties, ecological roles, and societal risks or benefits) is a key element in this process (Lima *et al.*, 2008). Identifications of fungi, even for experts, can be time consuming and made difficult with frequent revisions of the taxonomic schemes. In addition, each taxonomic group has specialised literature, terminology and characters (Santos *et al.*, 2008). This occurs to the extent that identifications can only be undertaken with a degree of reliability, by a small number of scientists skilled in the "art". The concept of species is clearly abstract; delimitations are very difficult and often not consensual. Taking this into account, microbial taxonomy (more evident in fungal taxonomy) and their associate data can often be best applied at the moment where the data are used a specific purpose: A pragmatic definition is "data fit for use". It is gradually becoming clearer that microbial identifications and authentication requires a polyphasic approach to generate quality data which are accurate and useful (Keys *et al.*, 2004). Recently, Matrix-Assisted Laser Desorption/Ionisation Time-Of-Flight Mass Spectrometry (MALDI-TOF MS) has been used to generate spectra of protein masses in the range of 2000 to 20000 Da that are taxon specific fingerprints (Kallow *et al.*, 2006). The advantages of this novel approach are the simple sample preparation procedure, short time (few minutes) for analysis and reliability of the data. The procedure is inexpensive (basically labour only) (Dickinson *et al.*, 2004) after purchase of the equipment. We will present and discuss our experience in the isolation, identification, preservation and distribution of strains from Nature of this important fungal taxon.

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